

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 04:46:06 ; Search time 37 Seconds
(without alignments)
522.430 Million cell updates/sec

Title: US-09-988-974-5

Sequence: 1062
1 MAGKSLFKVILLGSGVGK.....LIQDTVNLHKKPKSSSCC 201

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR_76: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

RESULT 1
G02361
small GTP binding protein Rab9 - human

C/Species: Homo sapiens (man)

C/Date: 06-Dec-1994 #sequence_revision 06-Jun-1997 #text_change 02-Feb-2001

C/Accession: G02361
R;Jannou, Y.A.; Davies, J.P.
submitted to the EMBL Data Library, December 1995

A/Reference number: H01115

A/Accession: G02361
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA
A/Residues: 1-201 <10A>

A/Cross-references: EMBL:U44103; NID:g1174146; PIDN:AACS1200.1; PID:g1174147
C/Superfamily: ras transforming protein; translation elongation factor Tu homology

C/Keywords: GTP binding; nucleotide binding; P-loop
F/8-127/Domain: translation elongation factor Tu homology <ETU>

F/14-21/Region: nucleotide-binding motif A (P-loop)
F/124-127/Region: GTP-binding NKXD motif
F/154-156/Region: GTP-binding SAK/L motif

Query Match 100.0%; Score 1062; DB 2; Length 201;

Best Local Similarity 100.0%; Pred. No. 1.6e-89;

Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGKSLFKVILLGSGVGKSLMNRVYTNKPDQLFHTIGVPLNKDLVDGHPVTMOI 60

Db 1 MAGKSLFKVILLGSGVGKSLMNRVYTNKPDQLFHTIGVPLNKDLVDGHPVTMOI 60

QY 61 WDTAGQERFRSLRTPPYRSGDCCLLTFSYVDSSQSFNLNMWKEFIYADVPESEFPV 120

Db 61 WDTAGQERFRSLRTPPYRSGDCCLLTFSYVDSSQSFNLNMWKEFIYADVPESEFPV 120

QY 121 ILGNKIDISERQVSTEEAQAQWCRDNGDYPYFESADATNVAAAFEAARVLATDRSD 180

Db 121 ILGNKIDISERQVSTEEAQAQWCRDNGDYPYFESADATNVAAAFEAARVLATDRSD 180

QY 181 HLIGDTVNLHKKPKSSSCC 201

Db 181 HLIGDTVNLHKKPKSSSCC 201

RESULT 2

S36187
GTP-binding protein rab9 - dog

C/Species: Canis lupus familiaris (dog)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Feb-2001

C/Accession: S36187; C36364; S15605; S37290
R;Lombardi, D.; Soldati, T.; Riederer, M.A.; Gada, Y.; Zerial, M.; Pfeiffer, S.R.

EMBL:U44103; NID:g1174146; PIDN:AACS1200.1; PID:g1174147
A/Title: Rab9 functions in transport between late endosomes and the trans Golgi network.
A/Reference number: S36187; MUID:93178443; PMID:8440258

A;Accession: S36187
A;Molecule type: mRNA
A;Residues: 1-201 <LOM>
A;Cross-references: EMBL:X56386
R;Chavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.
Mol. Cell. Biol. 10, 6578-6585, 1990
A;Title: Molecular cloning of FpII/SEC4-related cDNAs from an epithelial cell line.
A;Reference number: A36364; MUID:91061765; PMID:2123294
A;Accession: C36364
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 30-201 <CHA>
A;Cross-references: GB:X56386; NID:G2189; PIDN:CAA39797.1; PID:G2190
C;Genetics:
A;Gene: rab9
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; nucleotide binding; P-loop
F;8-127/Domain: translation elongation factor Tu homology <ETU>
F;14-21/Region: nucleotide-binding motif A (P-loop)
F;124-127/Region: GTP-binding NKXD motif
F;154-156/Region: GTP-binding SAK/L motif

Query Match 99.5%; Score 1057; DB 2; Length 201;
Best Local Similarity 99.5%; Pred. No. 4.5e-89;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAGKSSLFKVLILGDGGVGKSSLMNRYVTNKFTQTLFHTIGVEFLNKDLEVDGHHFTVMTQI 60	
DB	1	MAGKSSLFKVLILGDGGVGKSSLMNRYVTNKFTQTLFHTIGVEFLNKDLEVDGHHFTVMTQI 60	
QY	61	WDTAGQERFRSLRTPFYRGSDCCLLTFSDVDSQSFLNLSNWKKEFIYADVKPESEFPFV 120	
DB	61	WDTAGQERFRSLRTPFYRGSDCCLLTFSDVDSQSFLNLSNWKKEFIYADVKPESEFPFV 120	
QY	121	ILGNKIDISERQVSTEEAQAWCRDNGDYPYFETSADATNVAAPFEAVRVLATDRSD 180	
DB	121	ILGNKIDISERQVSTEEAQAWCRDNGDYPYFETSADATNVAAPFEAVRVLATDRSD 180	
QY	181	HLIQTDTVNLHRKPKPSSCC 201	
DB	181	HLIQTDTVNLHRKPKPSSCC 201	

QY 4]
DB 5]
QY
DB
QY
DB
QY
DB
QY
DB
RESUI
B3041
GTP-L
C;Spe
C;Dat
C;Acc
R;Cha
Mol.
A;Tit
A;Ref
A;ACC
A;Sta
A;Mol
A;Res
A;Cro
R;Cha
Cell
A;Tit
A;Ref
A;Acc
A;Sta
A;Mol
A;Res
A;Cro
A;Cro

BT 5
58
se Rab7 p
cies: HO
te: 04-Seq
ession:
elli, R.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 04:46:06 ; Search time 37 Seconds
(without alignments)
522.430 Million cell updates/sec

Title: US-09-988-974-5
Perfect score: 1062
Sequence: 1 MAGKSSLFKVLILGDGVGK.....LIQTDVNLHRKPKSSSCC 201

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database 1: PIR 76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1062	100.0	201	G02361	small GTP binding
2	1057	99.5	201	S36187	GTP-binding protei
3	533	50.2	206	JC4107	membrane vesicle t
4	529	49.8	207	B30413	GTP-binding protei
5	529	49.8	207	JC5268	GTPase Rab7 protei
6	527	49.6	207	S62733	small GTP-binding
7	526.5	49.6	201	S01934	GTP-binding protei
8	523.5	49.3	205	S36368	GTP-binding protei
9	523	49.2	206	S33531	GTP-binding protei
10	520.5	49.0	207	T12579	GTP-binding protei
11	518.5	48.8	209	T26119	hypothetical prote
12	515	48.5	205	T03529	GTP-binding protei
13	514	48.4	205	T40425	ras-related protei
14	514	48.4	206	T03628	GTP-binding protei
15	509	47.9	206	H96562	hypothetical prote
16	501.5	47.2	206	C96529	probable RAB7 GTP-
17	499.5	47.0	206	S39566	rab7 protein - soy
18	499	47.0	203	T00770	GTP-binding protei
19	498	46.9	204	T03630	GTP-binding protei
20	496.5	46.8	206	S39567	rab7 protein - mot
21	495	46.6	208	A44334	GTP-binding protei
22	493	46.4	208	T04019	rab7 protein homol
23	484.5	45.6	230	C84506	probable RAS type
24	373	35.1	216	JN0056	GTP-binding protei
25	373	35.1	216	C36364	GTP-binding protei
26	373	35.1	216	S47169	GTP-binding protei
27	369.5	34.8	216	JC4108	GTP-binding protei
28	368	34.7	214	SI0026	GTP-binding protei
29	359.5	33.9	202	S38740	GTP-binding protei

30	353	33.2	221	2	H71444	GTP-binding protei
31	352.5	33.2	203	2	S34253	GTP-binding protei
32	350	33.0	214	2	J50641	GTP-binding protei
33	349	32.9	218	2	C38625	GTP-binding protei
34	348	32.8	217	2	A86230	hypothetical prote
35	347	32.7	219	2	G84723	probable RAS type
36	346	32.6	218	2	JC2487	GTP-binding protei
37	346	32.6	218	2	A55005	GTP-binding protei
38	345	32.5	215	2	T06443	GTP-binding protei
39	344.5	32.4	217	2	S36365	GTP-binding protei
40	344	32.4	208	2	A38202	GTP-binding protei
41	343	32.3	202	2	S41430	GTP-binding protei
42	343	32.3	214	2	T14566	GTP-binding protei
43	341	32.1	211	2	T29035	hypothetical prote
44	341	32.1	223	2	S42679	GTP-binding protei
45	340.5	32.1	258	2	B86153	ARA-5 [imported]

ALIGNMENTS

RESULT 1

G02361
small GTP binding protein Rab9 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 02-Feb-2001
C:Accession: G02361
R.Ioannou, Y.A.; Davies, J.P.
submitted to the EMBL Data Library, December 1995
A:Reference number: H01115
A:Accession: G02361
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-201 <IC>
A:Cross-references: EMBL:U44103; NID:g1174146; PIDN:AC51200.1; PID:g1174147
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; nucleotide binding; P-loop
F:8-127/Domain: translation elongation factor Tu homology <ETU>
F:14-21/Region: nucleotide-binding motif A (P-loop)
F:124-127/Region: GTP-binding NKXD motif
F:154-156/Region: GTP-binding SAK/L motif

Query Match	100.0%	Score	1062	DB	2	Length	201
Best Local Similarity	100.0%	Pred. No.	1.6e-89				
Matches	201	Conservative	0	Mismatches	0	Indels	0
QY	1	MAGKSSLFKVLILGDGVGKSSLMNRVTYTNKFDLTQLEHTIGVEFLNKDLEVDGHFVTMQI	60				
Db	1	MAGKSSLFKVLILGDGVGKSSLMNRVTYTNKFDLTQLEHTIGVEFLNKDLEVDGHFVTMQI	60				
QY	61	WDTAGQERFRLRTPFYRGSDCCLLTFSDVDSQSFQNLNKKKEFIYADVKEPSPFV	120				
Db	61	WDTAGQERFRLRTPFYRGSDCCLLTFSDVDSQSFQNLNKKKEFIYADVKEPSPFV	120				
QY	121	ILGNKIDISERQVSTEEAQWCRDNGDYPYFESAKDATNVAAPFAEAVRVLATEDRSD	180				
Db	121	ILGNKIDISERQVSTEEAQWCRDNGDYPYFESAKDATNVAAPFAEAVRVLATEDRSD	180				
QY	181	HLIQTDVNLHRKPKSSSCC	201				
Db	181	HLIQTDVNLHRKPKSSSCC	201				

RESULT 2

S36187
GTP-binding protein rab9 - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Feb-2001
C:Accession: S36187; C36364; S15605; S37290
R.Lombardi, D.; Soldati, T.; Kiederer, M.A.; Goda, Y.; Zerial, M.; Pfeiffer, S.R.
EMBL:U127677-682/1993
A:Title: Rab9 functions in transport between late endosomes and the trans Golgi network.
A:Reference number: S36187; MUID:93178443; PMID:8440258

A:Accession: S36187

A:Molecule type: mRNA

A:Residues: 1-201 <LOM>

A:Cross-references: EMBL:X56386

R;Chavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.

Mol. Cell. Biol. 10, 6578-6585, 1990

A:Title: Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial cell line.

A:Reference number: A36364; MUID:91061765; PMID:2123294

A:Accession: C36364

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 30-201 <CHA>

A:Cross-references: GB:X56386; NID:g2189; PIDN:CAA39797.1; PID:g2190

C:Genetics:

A:Gene: rab9

C:Superfamily: ras transforming protein; translation elongation factor Tu homology

C:Keywords: GTP binding; nucleotide binding; P-loop

F:8-127/Domain: translation elongation factor Tu homology <ETU>

F:14-21/Region: nucleotide-binding motif A (P-loop)

F:124-127/Region: GTP-binding NKXD motif

F:154-156/Region: GTP-binding SAK/L motif

Query Match

Best Local Similarity 99.5%; Score 1057; DB 2; Length 201;

Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGKSLFKVILLGSGVCKSLMNRVYTNKFDTQLFHTIGVEFLNKOLEVDGHHVTMQI 60

Db 1 MAGKSLFKVILLGSGVCKSLMNRVYTNKFDTQLFHTIGVEFLNKOLEVDGHHVTMQI 60

QY 61 WTAGQERFSLRTFFRGSDCLLTFSVDDSQSQFQNLNNKKEFIYADVKEPSPFFV 120

Db 61 WTAGQERFSLRTFFRGSDCLLTFSVDDSQSQFQNLNNKKEFIYADVKEPSPFFV 120

QY 121 ILGNKIDISEROVSTEEAQAQRCDNGDYPYFETSADATNVAAPEEAVRVLATERSD 180

Db 121 ILGNKIDISEROVSTEEAQAQRCDNGDYPYFETSADATNVAAPEEAVRVLATERSD 180

QY 181 HLIQTDVNLHKKPKPSSCC 201

Db 181 HLIQTDVNLHKKPKPSSCC 201

RESULT 3

Membrane vesicle transport protein ypt C5 - Chlamydomonas reinhardtii

N:Alternate names: ras-like yptC5 protein; small G protein yptC5

C:Species: Chlamydomonas reinhardtii

C:Date: 21-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 02-Feb-2001

R;Dietmaier, W.; Fabry, S.; Huber, H.; Schmitt, R.

Gene 158, 41-50, 1995

A:Title: Analysis of a family of ypt genes and their products from Chlamydomonas reinhardtii

A:Reference number: J4105; MUID:95309723; PMID:7789809

A:Accession: J4107

A:Molecule type: mRNA

A:Residues: 1-206 <DIE>

A:Cross-references: GB:U13170; NID:g806725; PIDN:AAA82728.1; PID:g806726

C:Comment: This protein plays an essential role in the regulation of intracellular membrane

C:Genetics:

A:Gene: yptC5

A:Introns: 18/1; 60/3; 109/3; 136/3; 185/1

C:Superfamily: ras transforming protein; translation elongation factor Tu homology

C:Keywords: GTP binding; nucleotide binding; P-loop

F:9-128/Domain: translation elongation factor Tu homology <ETU>

F:15-22/Region: nucleotide-binding motif A (P-loop)

F:37-45/Domain: effector #status predicted <EFF>

F:125-128/Region: GTP-binding NKXD motif

F:158-160/Region: GTP-binding SAK/L motif

Query Match

Best Local Similarity 50.2%; Score 533; DB 2; Length 206;

Matches 105; Conservative 33; Mismatches 59; Indels 6; Gaps 3;

QY 4 KSSLFKVILLGSGVCKSLMNRVYTNKFDTQLFHTIGVEFLNKOLEVDGHHVTMQIWD 63

Db 5 KXRLLVIIILGSGVCKSLMNRVYTNKFDTQLFHTIGVEFLNKOLEVDGHHVTMQIWD 64

QY 64 AGQERFSLRTFFRGSDCLLTFSVDDSQSQFQNLNNKKEFIYADVKEPSPFFVILG 123

Db 65 AGQERFSLRTFFRGSDCLLTFSVDDSQSQFQNLNNKKEFIYADVKEPSPFFVILG 124

QY 124 NKIDI---SEROVSTEEAQAQRCDNGDYPYFETSADATNVAAPEEAVRVLATERSD 180

Db 125 NKIDENGSGSRQVSEKAKAWCKSGSPYFETSADATNVAAPEEAVRVLATERSD 183

QY 181 HLIQTDVNLH---RKPKPSSCC 201

Db 184 ELFMPPDAVDMNTTATQKRAQCC 206

RESULT 4

GTP-binding protein rab7 - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 02-Feb-2001

C:Accession: B30413; C39648

R;Chavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.

Mol. Cell. Biol. 10, 6578-6585, 1990

A:Title: Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial cell line.

A:Reference number: A36364; MUID:91061765; PMID:2123294

A:Accession: B30413

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-207 <CHA>

A:Cross-references: GB:M35522; NID:g164057; PIDN:AAA30890.1; PID:g164058

R;Chavrier, P.; Parton, R.G.; Hauri, H.P.; Simons, K.; Zerial, M.

Cell 62, 317-329, 1990

A:Title: Localization of low molecular weight GTP binding proteins to exocytic and endocytic

A:Reference number: A3648; MUID:90322428; PMID:2115402

A:Accession: C39648

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-207 <CH2>

A:Cross-references: GB:M35522; NID:g164057; PIDN:AAA30890.1; PID:g164058

C:Superfamily: ras transforming protein; translation elongation factor Tu homology

C:Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop

F:9-128/Domain: translation elongation factor Tu homology <ETU>

F:15-22/Region: nucleotide-binding motif A (P-loop)

F:125-128/Region: GTP-binding NKXD motif

F:155-157/Region: GTP-binding SAK/L motif

Query Match

Best Local Similarity 49.8%; Score 529; DB 2; Length 207;

Matches 98; Conservative 24; Mismatches 51; Indels 0; Gaps 0;

QY 4 KSSLFKVILLGSGVCKSLMNRVYTNKFDTQLFHTIGVEFLNKOLEVDGHHVTMQIWD 63

Db 5 KXRLLVIIILGSGVCKSLMNRVYTNKFDTQLFHTIGVEFLNKOLEVDGHHVTMQIWD 64

QY 64 AGQERFSLRTFFRGSDCLLTFSVDDSQSQFQNLNNKKEFIYADVKEPSPFFVILG 123

Db 65 AGQERFSLRTFFRGSDCLLTFSVDDSQSQFQNLNNKKEFIYADVKEPSPFFVILG 124

QY 124 NKIDISEROVSTEEAQAQRCDNGDYPYFETSADATNVAAPEEAVRVLATERSD 176

Db 125 NKIDLENROVATKRAQAWCYKNNIPYFETSADATNVAAPEEAVRVLATERSD 177

RESULT 5

GTPase Rab7 protein - human

C:Species: Homo sapiens (man)

C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 02-Feb-2001

C:Accession: J45268

R;Vitelli, R.; Chiarillo, M.; Lattero, D.; Bruni, C.B.; Bucci, C.

```

Biochem. Biophys. Res. Commun. 229, 887-890, 1996
A:Title: Molecular cloning and expression analysis of the human Rab7 GTP-ase complementa
A:Reference number: JC5268; MUID:97115674; PMID:8954989
A:Accession: JC5268
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-207 <VT>
A:Cross-references: EMBL:X93499; NID:g1089892; PIDN:CAA63763.1; PID:g1089893
A:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; nucleotide binding; P-loop
F:9-128/Domain: translation elongation factor Tu homology <ETU>
F:15-22/Region: nucleotide-binding motif A (P-loop)
F:125-128/Region: GTP-binding NKXD motif
F:155-157/Region: GTP-binding SAK/L motif

Query Match 49.8%; Score 529; DB 2; Length 207;
Best Local Similarity 56.6%; Pred. No. 7.1e-41;
Matches 98; Conservative 24; Mismatches 51; Indels 0; Gaps 0;

QY 4 KSSLFKVILLGDGGVKGSSLMNRYVYTNKFDPTQLFHTIGVFLNKDLEVDGHFVTMQIWDIT 63
Db 5 KKVLLKVIILGDSGVGKTSMLNQYVKNKFSNQYKATIGADFLTKENVVDRLVTMQIWDIT 64

QY 64 AGQRFSLRTPFYRGSDCCLLTFSVDDSSQFNLNWKKEFIYYADVKPESPFPVILG 123
Db 65 AGQRFOSLGVAFYRGADCCVLVDVTPNTFTKLSWRDEFLTQASPRDPENFPFVLG 124

QY 124 NKIDISEROVSTEEAQAACWCRDNGDYPYFETSADATNVAAPAEAVRVRLATE 176
Db 125 NKIDLENRQVATKRAQACWCKNIPYFETSADATNVAAPAEAVRVRLATE 177

RESULT 6
S62733
Small GTP-binding protein Rab7 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 02-Feb-2001
R:Vitelli, R.; Chiarliello, M.; Bruni, C.B.; Bucci, C.
Biochim. Biophys. Acta 1264, 268-270, 1995
A:Title: Cloning and expression analysis of the murine Rab7 cDNA.
A:Reference number: S62733; MUID:96138545; PMID:8547311
A:Accession: S62733
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-207 <VIT>
A:Cross-references: EMBL:X89650; NID:g1050550; PIDN:CAA61797.1; PID:g1050551
C:Genetics:
A:Gene: Rab7
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; nucleotide binding; P-loop
F:9-128/Domain: translation elongation factor Tu homology <ETU>
F:15-22/Region: nucleotide-binding motif A (P-loop)
F:125-128/Region: GTP-binding NKXD motif
F:155-157/Region: GTP-binding SAK/L motif

Query Match 49.6%; Score 527; DB 2; Length 207;
Best Local Similarity 56.6%; Pred. No. 1.1e-40;
Matches 98; Conservative 24; Mismatches 51; Indels 0; Gaps 0;

QY 4 KSSLFKVILLGDGGVKGSSLMNRYVYTNKFDPTQLFHTIGVFLNKDLEVDGHFVTMQIWDIT 63
Db 5 KKVLLKVIILGDSGVGKTSMLNQYVKNKFSNQYKATIGADFLTKENVVDRLVTMQIWDIT 64

QY 64 AGQRFSLRTPFYRGSDCCLLTFSVDDSSQFNLNWKKEFIYYADVKPESPFPVILG 123
Db 65 AGQRFOSLGVAFYRGADCCVLVDVTPNTFTKLSWRDEFLTQASPRDPENFPFVLG 124

QY 124 NKIDISEROVSTEEAQAACWCRDNGDYPYFETSADATNVAAPAEAVRVRLATE 176
Db 125 NKIDLENRQVATKRAQACWCKNIPYFETSADATNVAAPAEAVRVRLATE 177

```

RESULT 7

```

S01934
GTP-binding protein, 23K - rat
N:Alternate names: ras-related protein, 23K
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 02-Feb-2001
A:Accession: S01934
R:Bucci, C.; Frunzio, R.; Chiarliotti, L.; Brown, A.L.; Rehler, M.M.; Bruni, C.B.
Nucleic Acids Res. 16, 9979-9993, 1988
A:Title: A new member of the ras gene superfamily identified in a rat liver cell line.
A:Reference number: S01934; MUID:89057527; PMID:3057452
A:Accession: S01934
A:Molecule type: mRNA
A:Residues: 1-201 <BUC>
A:Cross-references: EMBL:X12535
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop
F:3-122/Domain: translation elongation factor Tu homology <ETU>
F:9-16/Region: nucleotide-binding motif A (P-loop)
F:119-129/Region: GTP-binding NKXD motif
F:149-151/Region: GTP-binding SAK/L motif

Query Match 49.6%; Score 526.5; DB 2; Length 201;
Best Local Similarity 50.5%; Pred. No. 1.2e-40;
Matches 100; Conservative 32; Mismatches 63; Indels 3; Gaps 1;

QY 7 LFKVILLGDGGVKGSSLMNRYVYTNKFDPTQLFHTIGVFLNKDLEVDGHFVTMQIWDITAGQ 66
Db 2 LKVIILGDSGVGKTSMLNQYVKNKFSNQYKATIGADFLTKENVVDRLVTMQIWDITAGQ 61

QY 67 ERFRSLRTPFYRGSDCCLLTFSVDDSSQFNLNWKKEFIYYADVKPESPFPVILGNKI 126
Db 62 ERFSQSLGVAFYRGADCCVLVDVTPNTFTKLSWRDEFLTQASPRDPENFPFVILGNKI 121

QY 127 DISERQVSTEEAQAACWCRDNGDYPYFETSADATNVAAPAEAVRVRLATE---DRSDHLI 183
Db 122 DLENRQVATKRAQACWCKNIPYFETSADATNVAAPAEAVRVRLATE---DRSDHLI 181

QY 184 OTDTVNLHRKPKPSSSCC 201
Db 182 EPKLDKNERAKASAES 199

RESULT 8
S36368
GTP-binding protein yptv5 - Volvox carteri
C:Species: Volvox carteri
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Feb-2001
A:Accession: S36368
R:Fabry, S.; Jacobsen, A.; Huber, H.; Palme, K.; Schmitt, R.
Curr. Genet. 24, 229-240, 1993
A:Title: Structure, expression, and phylogenetic relationships of a family of ypt genes
A:Reference number: S36365; MUID:94037148; PMID:8221932
A:Accession: S36368
A:Molecule type: DNA
A:Residues: 1-205 <FAB>
A:Cross-references: GB:L08131; NID:g409167; PIDN:AAA34254.1; PID:g409168
C:Genetics:
A:Gene: Yptv5
A:Introns: 18/2; 60/3; 109/3; 135/3; 184/2
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; nucleotide binding; P-loop
F:9-128/Domain: translation elongation factor Tu homology <ETU>
F:15-22/Region: nucleotide-binding motif A (P-loop)
F:61-67/Region: GTP binding #status predicted
F:122-129/Region: GTP binding #status predicted
F:150-156/Region: GTP binding #status predicted

Query Match 49.3%; Score 523.5; DB 2; Length 205;
Best Local Similarity 50.5%; Pred. No. 2.2e-40;
Matches 102; Conservative 34; Mismatches 61; Indels 5; Gaps 3;

QY 4 KSSLFKVILLGDGGVKGSSLMNRYVYTNKFDPTQLFHTIGVFLNKDLEVDGHFVTMQIWDIT 63

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Db 5 KRVLVKIIILGDSGVGKTSIMNQYQKFTKEYKATIGADFLTKIEVDKDKVTMQIWD 64
QY 64 AGQERFSLRTPFYRGSDCLLTFSDSQFNLNNKKEFIYADVKEPESPPFVILG 123
Db 65 AGQERFQSLGSAFYRGADCCMLVFNNAKSFDDLDNRDEFILQAGSPDPNPFVILG 124
QY 124 NKIDI--SERQVSTEEAQAACRNDGDPYFETSAKDNTNVAFAEAVRRVLATEDRSDH 181
Db 125 NKIDVGNVRQVTEKKAKAWCAKSGSIPYFETSAKEDINVEAFTCIETNALRNE-KEEE 183
QY 182 LIQTDTVNLHRK--PKPSSSC 201
Db 184 LFPDADVMNTSATORKRGCC 205

RESULT 9

S33531
GTP-binding protein rab - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Feb-2001
C:Accession: S33531; S25543
R:Drew, J.E.; Bown, D.; Gatehouse, J.A.
Plant Mol. Biol. 21, 1195-1199, 1993
A:Title: Sequence of a novel plant ras-related cDNA from Pisum sativum.
A:Reference number: S33531; MUID:93257636; PMID:8490139
A:Accession: S33531
A:Molecule type: mRNA
A:Residues: 1-206 <DRE>
A:Cross-references: EMBL:X65650; NID:G20755; PIDN:CAA46600.1; PID:G20756
A>Note: the authors translated the codon AAA for residue 48 as Thr, and CCC for residue
C:Genetic:
A:Gene: rab
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; nucleotide binding; P-loop
F:9-128/Domain: translation elongation factor Tu homology <ETU>
F:15-22/Region: nucleotide-binding motif A (P-loop)
F:125-128/Region: GTP-binding NXXD motif
F:158-160/Region: GTP-binding SAK/L motif

Query Match 49.2%; Score 523; DB 2; Length 206;
Best Local Similarity 48.3%; Pred. No. 2.5e-40;
Matches 97; Conservative 42; Mismatches 58; Indels 4; Gaps 2;

QY 4 KSSLFKVILLGDSGVGKTSIMNQYQKFTKEYKATIGADFLTKIEVDKDKVTMQIWD 63
Db 5 RRTLLKVIILGDSGVGKTSIMNQYQKFTKEYKATIGADFLTKIEVDKDKVTMQIWD 64
QY 64 AGQERFSLRTPFYRGSDCLLTFSDSQFNLNNKKEFIYADVKEPESPPFVILG 123
Db 65 AGQERFQSLGSAFYRGADCCMLVFNNAKSFDDLDNRDEFILQAGSPDPNPFVILG 124
QY 124 NKIDI--SERQVSTEEAQAACRNDGDPYFETSAKDNTNVAFAEAVRRVLATEDRSD 180
Db 125 NKIDVGNVRQVTEKKAKAWCAKSGSIPYFETSAKEDINVEAFTCIETNALRNE-KEEE 183
QY 182 LIQTDTVNLHRK--PKPSSSC 201
Db 184 LFPDADVMNTSATORKRGCC 205

RESULT 10

T12579
GTP-binding protein Rab7a - common ice plant
C:Species: Mesembryanthemum crystallinum (common ice plant)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jan-2000
C:Accession: T12579
R:Michalowski, C.B.; Bohnert, H.J.
Submitted to the EMBL Data Library, January 1997
A:Description: Sequence of a GTP-binding protein from Mesembryanthemum crystallinum.
A:Reference number: T12579
A:Accession: T12579
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-207 <MIC>
A:Cross-references: EMBL:U97142; NID:G1842068; PID:G1842069
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; P-loop
F:9-128/Domain: translation elongation factor Tu homology <ETU>

Query Match 49.0%; Score 520.5; DB 2; Length 207;
Best Local Similarity 48.5%; Pred. No. 4.2e-40;
Matches 98; Conservative 41; Mismatches 58; Indels 5; Gaps 3;

QY 4 KSSLFKVILLGDSGVGKTSIMNQYQKFTKEYKATIGADFLTKIEVDKDKVTMQIWD 63
Db 5 RRTLLKVIILGDSGVGKTSIMNQYQKFTKEYKATIGADFLTKIEVDKDKVTMQIWD 64
QY 64 AGQERFSLRTPFYRGSDCLLTFSDSQFNLNNKKEFIYADVKEPESPPFVILG 123
Db 65 AGQERFQSLGSAFYRGADCCMLVFNNAKSFDDLDNRDEFILQAGSPDPNPFVILG 124
QY 124 NKIDI--SERQVSTEEAQAACRNDGDPYFETSAKDNTNVAFAEAVRRVLATEDRSD 180
Db 125 NKIDVGNVRQVTEKKAKAWCAKSGSIPYFETSAKEDINVEAFTCIETNALRNE-KEEE 184
QY 182 LIQTDTVNLHRK--PKPSSSC 201
Db 185 TYL-PDTIDMAGSTRPQSSAC 205

RESULT 11

T26119
hypothetical protein W03C9.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T26119
R:Gregory, J.; Ainscough, R.
Submitted to the EMBL Data Library, October 1995
A:Reference number: Z20155
A:Accession: T26119
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-209 <WIL>
A:Cross-references: EMBL:Z66516; PIDN:CAA91357.1; GSPDB:GN00020; CESP:W03C9.3
A:Experimental source: clone W03C9
C:Genetics:
A:Gene: CESP:W03C9.3
A:Map position: 2
A:Introns: 39/3; 61/3; 112/2; 181/3
C:Superfamily: ras transforming protein; translation elongation factor Tu homology

Query Match 48.8%; Score 518.5; DB 2; Length 209;
Best Local Similarity 48.8%; Pred. No. 6.5e-40;
Matches 101; Conservative 43; Mismatches 56; Indels 7; Gaps 4;

QY 1 MAG--KSSLFKVILLGDSGVGKTSIMNQYQKFTKEYKATIGADFLTKIEVDKDKVTMQIWD 58
Db 1 MSGTRKALLKVIILGDSGVGKTSIMNQYQKFTKEYKATIGADFLTKIEVDKDKVTMQIWD 60
QY 59 QIWDTAGQERFSLRTPFYRGSDCLLTFSDSQFNLNNKKEFIYADVKEPESPP 118
Db 61 QIWDTAGQERFQSLGSAFYRGADCCMLVFNNAKSFDDLDNRDEFILQAGSPDPNPFVILG 120
QY 119 FVILGNKIDI--SERQVSTEEAQAACRNDGDPYFETSAKDNTNVAFAEAVRRVLATE- 176
Db 121 FVILGNKIDLESQRAVSSKRAQWCQTKGNI-PYVESAKALNVEAFLATARDALAES 180
QY 177 -DRSDHLTQDTVNL--HRKPKPSSSC 200
Db 181 QETNDFPEFPDQIRLNPQNQQNSGC 207

RESULT 12

T03629
GTP-binding protein Rab7b - common tobacco

C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001
C;Accession: T03629
R;Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.
Plant Physiol. 108, 59-67, 1995
A;Title: Characterization of membrane-bound small GTP-binding proteins from Nicotiana glauca
A;Reference number: Z14896; MUID:95303981; PMID:7784525
A;Accession: T03629
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-205 <HAI>
A;Cross-references: EMBL:L29275; NID:g623589; PIDN:AAA74119.1; PID:g623590
A;Experimental source: strain SR1
C;Genetics:
A;Gene: Rab7b
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; nucleotide binding; P-loop
F;8-127/Domain: translation elongation factor Tu homology <ETU>
F;14-21/Region: nucleotide-binding motif A (P-loop)
F;124-127/Region: GTP-binding NKXD motif
F;157-159/Region: GTP-binding SAK/L motif

Query Match 48.5%; Score 515; DB 2; Length 205;
Best Local Similarity 46.6%; Pred. No. 1.3e-39;
Matches 95; Conservative 44; Mismatches 61; Indels 4; Gaps 2;

QY 1 MAGKSSLFKVILLGDGGVGKSSLMMRVVTNKFTQLFHTIGVEFLNKDLVDGHFVMTQI 60
Db :
Dy 1 MPSPANVLKVIILGDSGVGKTSIMNQVNKKFNQYKATIGADFLTKEVFDRLETLQI 60
Db :
Qy 61 WDTAGQERFSRLTFFRGSDCLLTFSDDSQSFQNLGNWKKFEITYYADVKEPESEFPFV 120
Db :
Qy 61 WDTAGQERFOSLGVAFYRGADCVCVLYVDVNSMKSFENLNWRREEFLIQASPSDPENFPFV 120
Db :
Qy 121 ILGNKIDI ---SRQVSTEEAQACWDNGDYPFETS AKDATNVAAAFEAARVRULATED 177
Db :
Qy 121 VLGNKDVIDGNSGRVVSEKKARAWCAKSGKNIPYFETSAKEGTVEEFAFCIAKNALKSGE 180
Db :
Qy 178 RSDHLITQDTWNLRHKPKPSSSCC 201
Db 181 -EEEIVPLDLDVGTSSQRTGC 203

RESULT 13
T04025
ras-related protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C;Accession: T40425
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21928
A;Accession: T40425
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-205 <SEE>
A;Cross-references: EMBL:AL035655; PIDN:CAB386603.1; GSPDB:GN00067; SPDB:SPBC405.04C
A;Experimental source: strain 972H-; cosmid c405
C;Genetics:
A;Gene: SPDB:SPBC405.04C
A;Map position: 2
A;Introns: 27/3; 135/3
C;Superfamily: ras transforming protein; translation elongation factor Tu homology

Query Match 48.4%; Score 514; DB 2; Length 205;
Best Local Similarity 48.8%; Pred. No. 1.6e-39;
Matches 100; Conservative 37; Mismatches 64; Indels 4; Gaps 3;

QY 1 MAGKSS-LFKVILLGDGGVGKSSLMMRVVTNKFTQLFHTIGVEFLNKDLVDGHFVMTQ 59
Db :
Dy 1 MAGKXHLKVIILGESGVGKTSIMNQYNRKFSKYKATIGADFLTKEVLVDKVKVTLQ 60
Db :
Qy 60 IWDTAGQERFSRLTFFRGSDCLLTFSDDSQSFQNLGNWKKFEITYYADVKEPESEFPF 119

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96562
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <STO>
A:Cross-references: GB:AE005173; NID:G10645452; PIDN:AAG21568.1; GSPDB:GN00141
C:Genetics:
A:Gene: F19K6.10
A:Map position: 1
C:Superfamily: ras transforming protein; translation elongation factor Tu homology

Query Match 47.9%; Score 509; DB 2; Length 206;
Best Local Similarity 48.5%; Pred. No. 4.7e-39;
Matches 96; Conservative 37; Mismatches 61; Indels 4; Gaps 2;
QY 7 LFKVILLGDSGVKSLMNRVYTNKPTQLFHTIGVEFLNKLVDGHEFTVNTQIWDTAGQ 66
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
8 LLKVIILGDSGVKTSILNQFVNRKFSNQYKATIGADFLTKVQIDDRIFTLIQIWDTAGQ 67
QY 67 ERFRLRTPFYRGSDCLLTFVSVDSDSQFNLNNWKEFIYYADVKEPESFPFVILGNKI 126
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
68 ERFQSLGVAFYRGADCCVLVIDVNVWKSFDNLNNWKEFLIQSPSDPENFPFVILGNKT 127
QY 127 DI--SEROVSTEEAQACWRDNGDYPFYFETSAKDATNVAAPFEAAVRYVLATEDRSDHLI 183
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
128 DVDGKSRVYVEKKAKAWCASKGNIPFYFETSAKEGPNVDAFECITKNAFKNEPEEPYL 187
QY 184 QTDVNLHRKPKPSSSCC 201
Db :||:||||:| :||:||||:| :||:||||:| :||:||||:|
188 -PTIDVAGGQQORSTGC 204

Search completed: February 10, 2004, 04:59:00
Job time : 39 secs